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Combining a process based model with a functional structural plant model for production partitioning and visualization

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Introduction

Process Based Models (PBM) are used to compute crop yield, they treat a field as a homogenous medium, total production is computed accurately, but there is little information on individual variability of plants, and number and size of organs. Functional Structural Plant Models (FSPM) simulate individual plant development and growth, they build plant architecture on the basis of biomass production and partitioning according to botanical rules, but generally lack the ability to upscale to the field level to address crop production. In the present study we combined crop biomass production of maize estimated by the PBM PILOTE with biomass partitioning and individual plant architecture generated by the FSPM GreenLab, in order to benefit from the field-level accuracy of the former and from the heterogeneity of individual architecture of the latter.

Model description and comparison

PILOTE (Mailhol et al., 1997) is a model designed for crop yield simulation. GreenLab (Guo et al., 2006) is an FSPM designed for individual plant architectural development and biomass partitioning. Although GreenLab and PILOTE address different scales, they take into account similar processes for biomass computation, based on Beer's Law for light interception (Table 1).

Table 1. Comparison of biomass computation by PILOTE and GreenLab

PILOTE (PBM)	GreenLab (FSPM)
$Q = RUE \cdot \sum_{\text{sowing}}^{\text{harvest}} PAR_{(i)} \cdot \left(1 - e^{-k \cdot LAI_{(i, \text{stress})}}\right) \text{ (Eq.1)}$	$q_{(n)} = \frac{RUE_{(n)} \cdot PAR_{(n)} \cdot Sp}{r} \left(1 - \exp\left(-k \cdot \frac{Sa_{(n)}}{Sp}\right)\right) \text{ (Eq.2)}$
<i>Q</i> : final total dry matter (t ha ⁻¹)	<i>q</i> : total biomass of individual plant at GC <i>n</i> (g)
<i>RUE</i> : radiation use efficiency	<i>RUE</i> : radiation use efficiency
<i>PAR</i> : daily photosynthetically active radiation (J m ⁻²)	<i>PAR</i> : photosynthetically active radiation at GC <i>n</i> (J m ⁻²)
<i>k</i> : extinction factor	<i>k</i> : extinction factor
<i>LAI</i> : daily <i>LAI</i> according to water stress (m ² m ⁻²)	<i>Sa</i> : total area of living leaves (cm ²)
sowing: sowing day of year	<i>Sp</i> : theoretic projection surface (cm ²)
harvest: harvest day of year	<i>r</i> : resistance to water transpiration
<i>i</i> : day <i>i</i>	<i>n</i> : current growth cycle ("GC")

The differences between the two models come from different spatio-temporal scales: PILOTE addresses plant population per unit area, GreenLab addresses individual plants. PILOTE computation is on a daily basis, GreenLab computation is by growth cycle (GC), based on thermal time. *LAI* in GreenLab is optimized by *Sa/Sp* ratio for an individual plant: leaf area is estimated from the source-sink balance, and the projection surface *Sp* is computed by multi-fitting and Eq.2 inversion (Ma et al., 2008). If the field is homogeneous, the *LAI* and total biomass computed by both models should be identical; on the contrary, if the results are different, it could be explained by field heterogeneity.

Field experiment

Measurements were conducted in 2009 at the Cemagref experimental station (Montpellier, FR). Maize (Pioneer PR35Y65) was sown on April 23 at 75000 plants per ha. The irrigation protocol involved surface drip irrigation, irrigation dates were adjusted on the basis of tensiometer monitoring and neutron probe measurements to avoid drainage risk and supply a water amount of 350 mm. LAI was monitored weekly during the cropping cycle, using a LAI2000 (LI-COR). For PILOTE calibration, plant samples were collected after maturity for evaluating total above ground dry matter and grain yield. For GreenLab calibration, observations were made on May 25, June 8, June 25, July 15 and July 30, each time 6 plants were harvested. Fresh weights of all organs (blade, petiole, internode, tassel and spike) were measured for each phytomer.

Model Calibration Results

Grain yield and total dry matter were accurately simulated by PILOTE (Fig. 1), confirming the good performance of the model previously established by Khaledian et al. (2009). Based on phytomer measurements, parameter fitting in GreenLab provided a satisfactory result (Fig. 2).

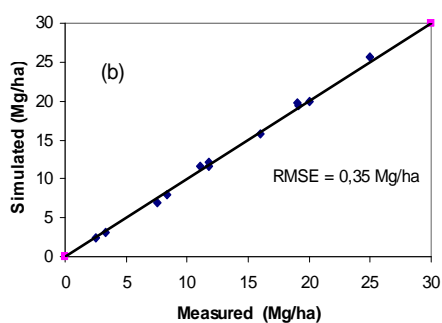


Fig. 1. Maize yield simulated by PILOTE

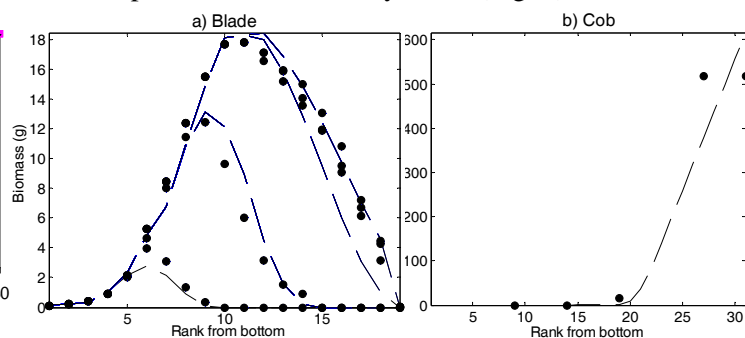


Fig. 2. Multi-fitting result of Maize by GreenLab

Analysis and Model Combination

In a first step, the results of total biomass and LAI simulated by both models were compared on the same scale (individual plant) and time step (growth cycle), all plants being assumed identical for GreenLab computation (Fig.3, PILOTE and GL_a). The total biomass and LAI computed with GreenLab (GL_a) displayed an earlier start and a steeper slope compared to PILOTE results.

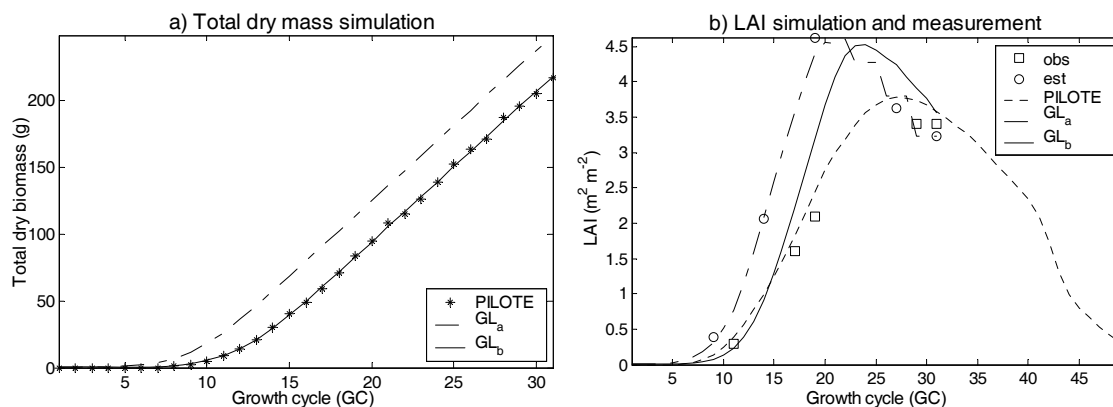


Fig. 3. Biomass and LAI output from PILOTE and GreenLab

GL_a : GreenLab simulation with all plants identical.

GL_b : GreenLab simulation with different germination dates.

obs : LAI observed from field measurement.

est : individual LAI computed by fresh mass measurement and estimated leaf thickness.

Within a field, individual growth of plants is however known to be heterogeneous, in particular concerning seedling emergence (Pommel et al., 2002). In a second step we considered a heterogeneity in germination date. We modelled a distribution of germination date (ranging from 1 to 8 GC) with a beta law function, fitted by least squares method (Fig.4). The resulting growth curves were then very close (Fig.3, GL_b). An example of architectural development of an individual maize plant is shown in Fig. 5.

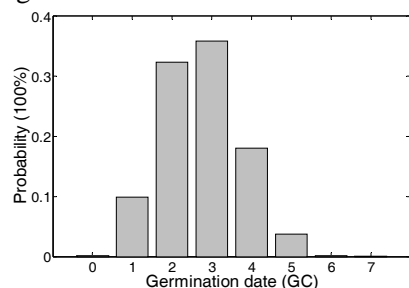


Fig. 4. Distribution of germination date



Fig. 5. Simulated maize architectural development

Discussion and Conclusion

PBMs and FSPMs both play important roles in agricultural studies and have their respective advantages, and cooperation between them can bring new opportunities in study methods and applications. In Fig. 3 there is still a slight discrepancy for leaf area estimation, despite the very good fit for total biomass. This can be attributed *i)* to the error in LAI measurement with a plant canopy analyzer, due to a heterogeneous plant cover, and *ii)* to the error in leaf thickness used for individual leaf area computation, which was done by allometry and not directly measured. Further work will seek to improve these estimations. Despite this uncertainty, the present work shows that the 3D architecture of a field can be successfully built based jointly on a PBM output and the knowledge and information from an FSPM. The former, offering a very good performance for total yield estimation, can help to calibrate the latter, which in return can account for individual spatial and/or temporal heterogeneity. From a crop production curve to plant individual 3D architecture according to growth stages, several opportunities in agricultural production optimization can be foreseen for the future, in addition to field and landscape visualization. Focusing on providing architectures for PBM from FSPM, this study will continue on other plants (wheat, sunflower, etc.), based on combination with other PBMs.

Acknowledgments

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